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Fig. 1 IgE amino acid surface exposure using the Padlan and Davies 1986 model.

Residue	Surface Area	average/5	> 50	> 80	
ARG_1	270.322723				
ASP_2	139.374542				
PHE_3	64.298927	117.361489	1	1	
THR_4	46.170193	64.494911	1	0	
PRO_5	66.64106	39.0209532	0	0	
PRO_6	5.989833	29.3644934	0	0	
THR_7	12.004753	21.4426604	0	0	
VAL_8	16.016628	8.6200336	0	0	
LYS_9	6.561028	10.2708042	0	0	
ILE_10	2.527926	9.5044914	0	0	
LEU_11	14.243686	13.375776	0	0	
GLN_12	8.173189	19.2992118	0	0	
SER_13	35.373051	29.1890154	0	0	
SER_14	36.178207	32.6313328	0	0	
CYS_15	51.976944	39.0100884	0	0	
ASP_16	31.455273	45.6135238	0	0	
GLY_17	40.066967	50.0871888	1	0	
GLY_18	68.390228	46.9957994	0	0	
GLY_19	58.546532	59.6253914	1	0	P5
HIS_20	36.519997	63.4215874	1	0	P5
PHE_21	94.603233	68.1998406	1	0	P5
PRO_22	59.047947	65.8523506	1	0	P5
PRO_23	92.281494	62.0824146	1	0	P5
THR_24	46.809082	50.1635586	1	0	P5
ILE_25	17.670317	38.6392736	0	0	
GLN_26	35.008953	21.6261078	0	0	
LEU_27	1.426522	12.5259452	0	0	
LEU_28	7.215665	10.5518628	0	0	
CYS_29	1.308269	3.5500722	0	0	
LEU_30	7.799905	4.8164434	0	0	
VAL_31	0	4.0672202	0	0	
SER_32	7.758378	3.8055664	0	0	
GLY_33	3.469549	9.5755666	0	0	
TYR_34	0	20.7786542	0	0	
THR_35	36.649906	28.9967052	0	0	
PRO_36	56.015438	50.2230378	1	0	P6
GLY_37	48.848633	57.590085	1	0	P6
THR_38	109.601212	73.50021	1	0	P6
ILE_39	36.835236	70.1846368	1	0	P6
ASN_40	116.200531	73.2560022	1	0	P6
ILE_41	39.437572	51.7217026	1	0	P6
THR_42	64.20546	49.2710734	0	0	
TRP_43	1.929714	35.2314448	0	0	
LEU_44	24.58209	49.7665942	0	0	
GLU_45	46.002388	50.9119188	1	0	
ASP_46	112.113319	74.3084848	1	0	
GLY_47	69.932083	91.0816862	1	1	
GLN_48	118.912544	85.9516244	1	1	P1
VAL_49	108.448097	91.6210626	1	1	

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TCTT" 884T650

MET_50	20.352079	89.4386316	1	1
ASP_51	140.46051	77.095856	1	0
VAL_52	59.019928	65.664336	1	0
ASP_53	57.198666	72.8180802	1	0
LEU_54	51.290497	45.9930286	0	0
SER_55	56.1208	49.3437382	0	0
THR_56	6.335252	47.723164	0	0
ALA_57	75.773476	43.8934994	0	0
SER_58	49.095795	51.656078	1	0
THR_59	32.142174	59.4056414	1	0
THR_60	94.933693	72.6291262	1	0
GLN_61	45.083069	73.3905916	1	0
GLU_62	141.8909	99.7907822	1	0 P2
GLY_63	52.903122	90.626043	1	1
GLU_64	164.143127	83.4067496	1	1
LEU_65	49.109997	57.2201384	1	1
ALA_66	8.986602	47.5504318	0	0
SER_67	10.957844	17.0083172	0	0
THR_68	4.554589	7.3021006	0	0
GLN_69	11.432554	7.2534874	0	0
SER_70	0.578914	5.0619186	0	0
GLU_71	8.743536	8.9567614	0	0
LEU_72	0	10.8120506	0	0
THR_73	24.028803	23.2812776	0	0
LEU_74	20.709	37.264713	0	0
SER_75	62.925049	69.375269	1	0
GLN_76	78.660713	79.6644746	1	0
LYS_77	160.55278	78.1594206	1	0
HIS_78	75.474831	77.9196576	1	0
TRP_79	13.18373	76.6092892	1	0 P3
LEU_80	61.726234	70.354977	1	0
SER_81	72.108871	73.244224	1	0
ASP_82	129.281219	81.9731098	1	1
ARG_83	89.921066	69.9061278	1	0
THR_84	56.828159	58.6259284	1	0
TYR_85	1.391324	32.7696846	0	0
THR_86	15.707874	23.8688072	0	0
CYS_87	0	12.5031754	0	0
GLN_88	45.416679	24.6922706	0	0
VAL_89	0	22.314276	0	0
THR_90	62.3368	48.4045714	0	0
TYR_91	3.817901	45.5941352	0	0
GLN_92	130.451477	47.9061642	0	0
GLY_93	31.364498	62.7324992	1	0
HIS_94	11.560145	91.805003	1	1
THR_95	136.468475	85.5324108	1	1
PHE_96	149.18042	87.190961	1	1
GLU_97	99.088516	90.6138422	1	1
ASP_98	39.657249	75.8683994	1	0
SER_99	28.674551	62.1985202	1	0
THR_100	62.741261	62.538042	1	0
LYS_101	80.831024	61.892236	1	0
LYS_102	100.786125	65.3434144	1	0 P4
CYS_103	36.428219	66.2248162	1	0
ALA_104	45.930443	63.0386422	1	0
ASP_105	67.14827	64.611715	1	0

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WO 00/50460

SER_106

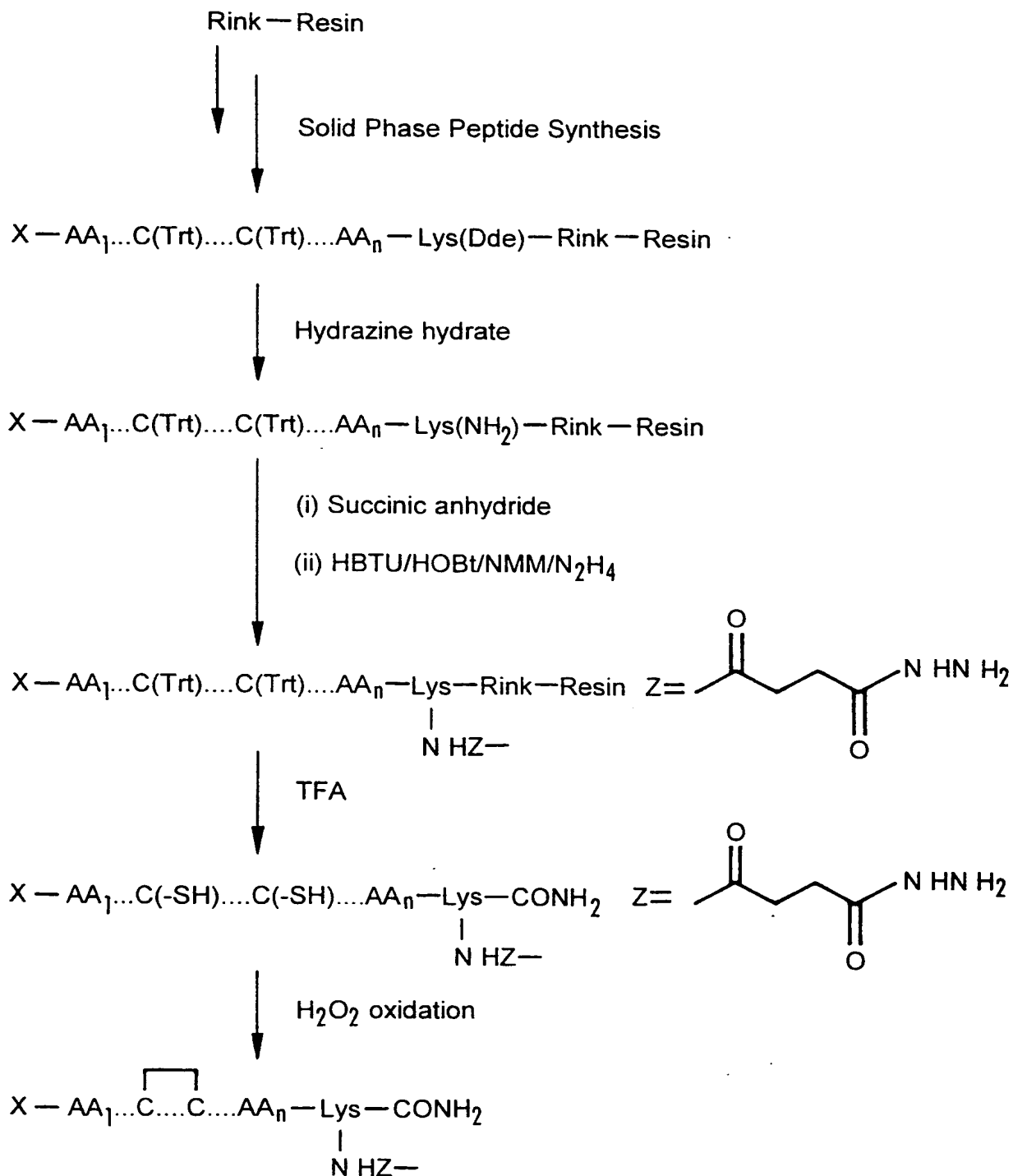
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1

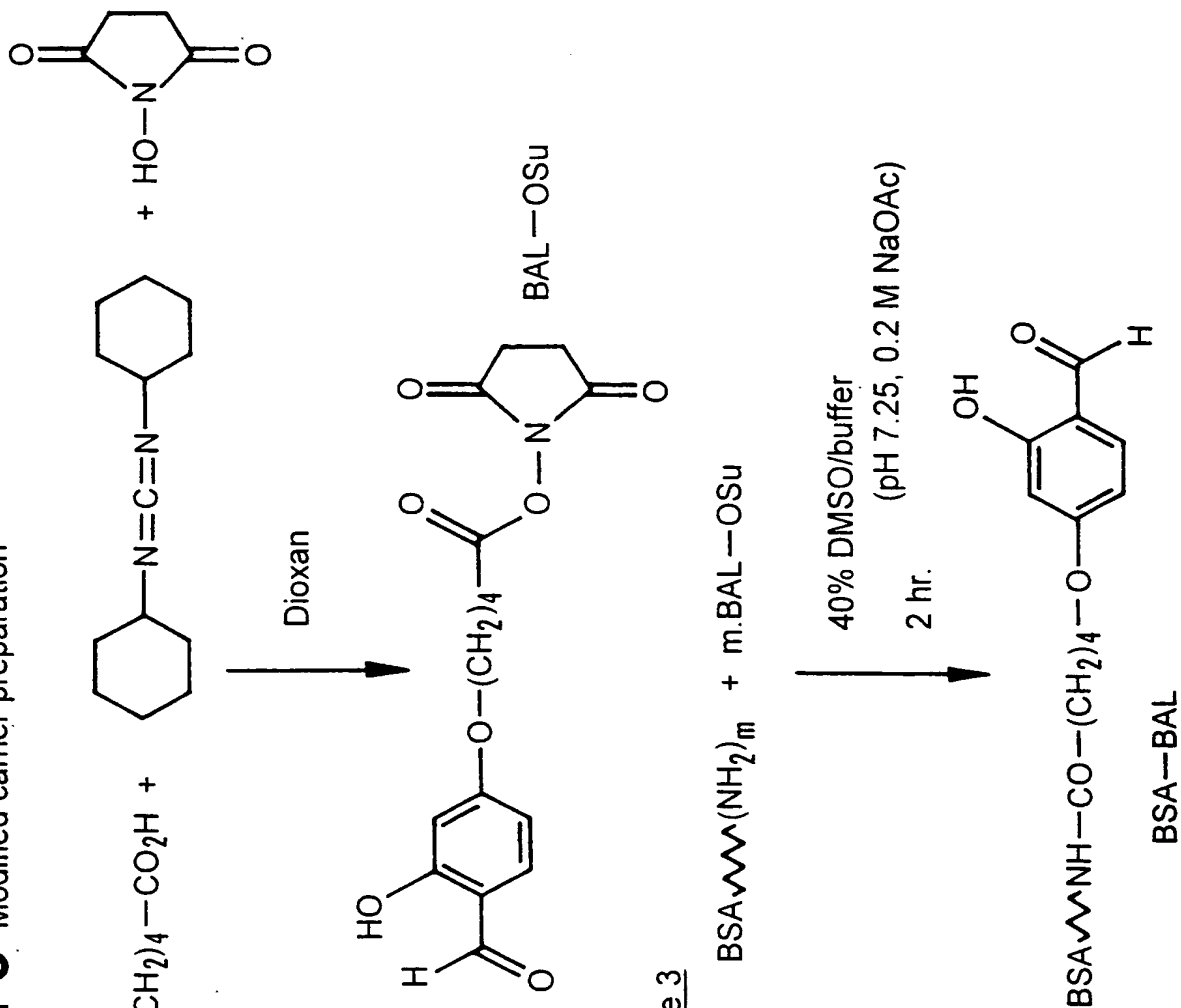
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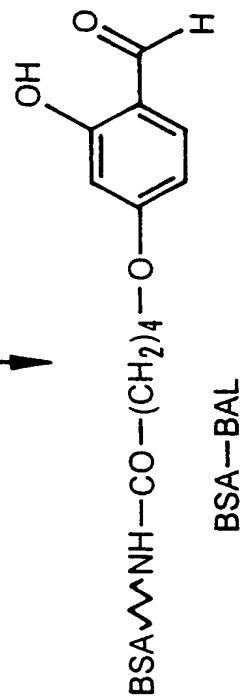
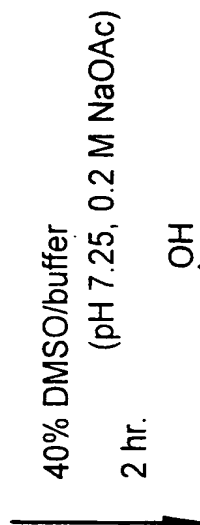
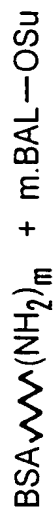
Fig. 2 Scheme 1, solid phase peptide synthesisScheme 1

Scheme 2

Fig. 3 Modified carrier preparation

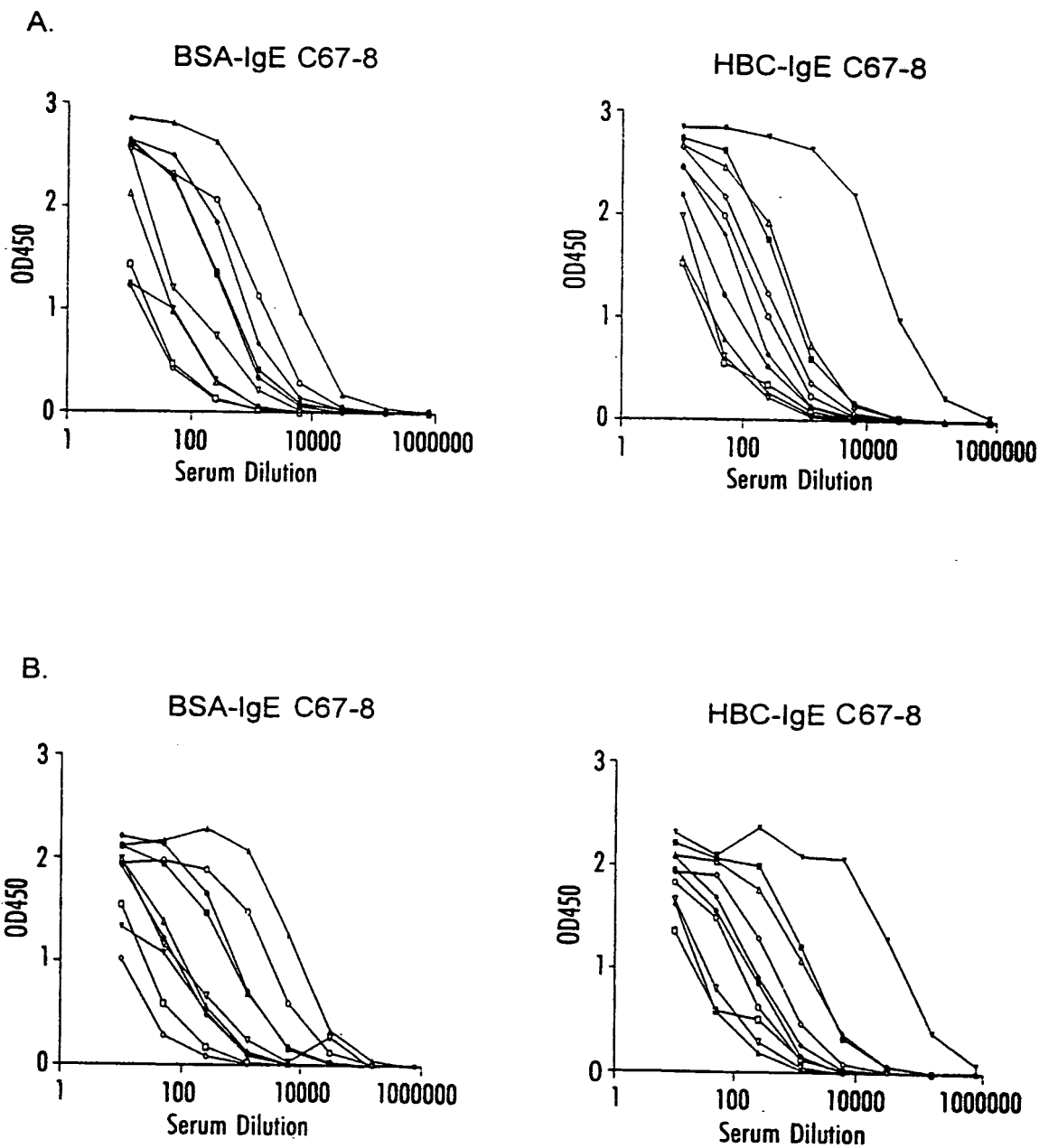


Scheme 3



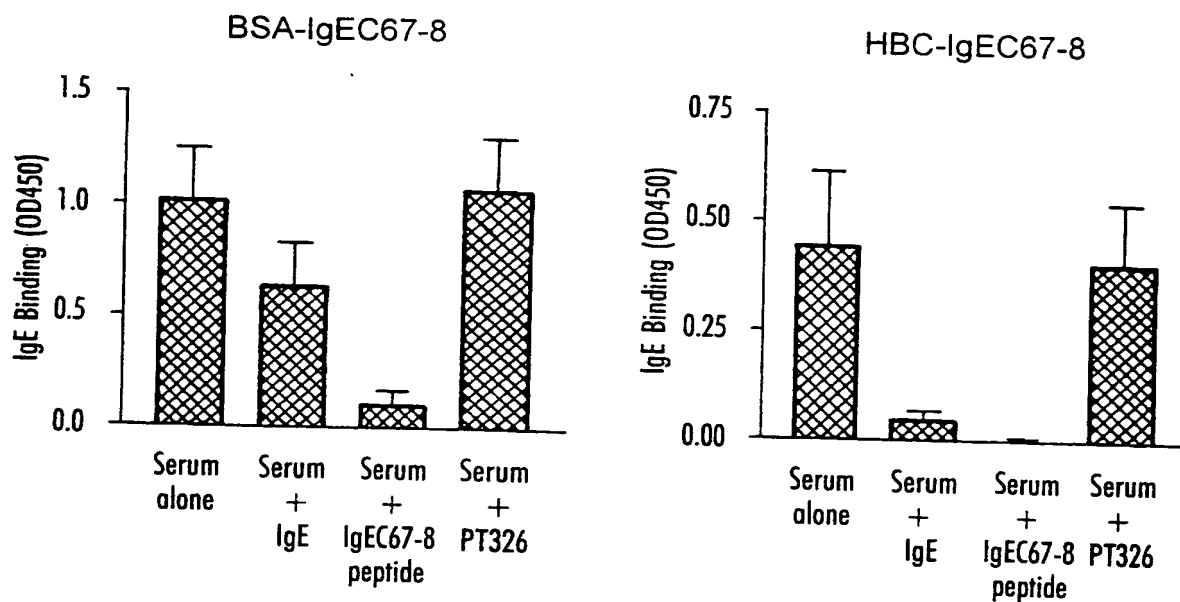
$$\begin{array}{c}
 \text{BSA} - \left[\text{O}-\text{C}_6\text{H}_3(\text{OH})-\text{CHO} \right]_m + 3 m \quad \text{X-AA}_1 \dots \text{C} \dots \text{C} \dots \text{AA}_n - \underset{\text{NH-Z}}{\text{Lys}} - \text{CONH}_2 \\
 \text{BSA-BAL} \\
 \downarrow \begin{array}{l} \text{50\% DMSO/buffer} \\ (\text{pH } 3.5, 0.1 \text{ M NaHCO}_2) \\ \sim 8-16 \text{ hr.} \end{array} \\
 \text{BSA} - \left[\text{O}-\text{C}_6\text{H}_3(\text{OH})-\text{CH=N-NH-C(=O)-CH}_2\text{-CH}_2\text{-C(=O)-NH-Lys}\dots\text{AA}_n\dots\text{C}\dots\text{C}\dots\text{AA}_1\text{-X} \right]_m
 \end{array}$$

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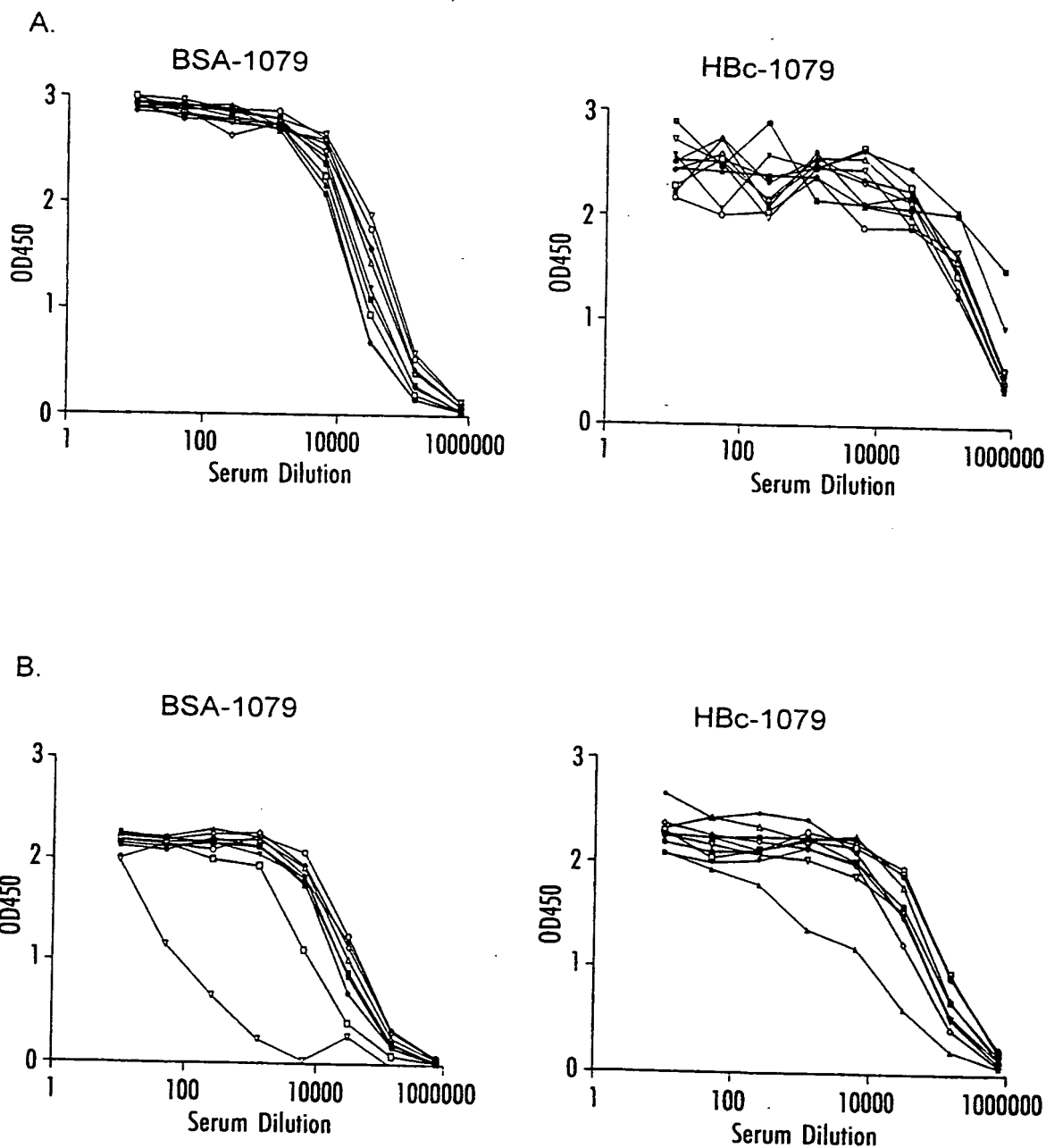
Fig. 5 C67-8 Anti-IgE Data

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Fig. 6 Competition assay with soluble IgE and IgE C67-8 peptide.

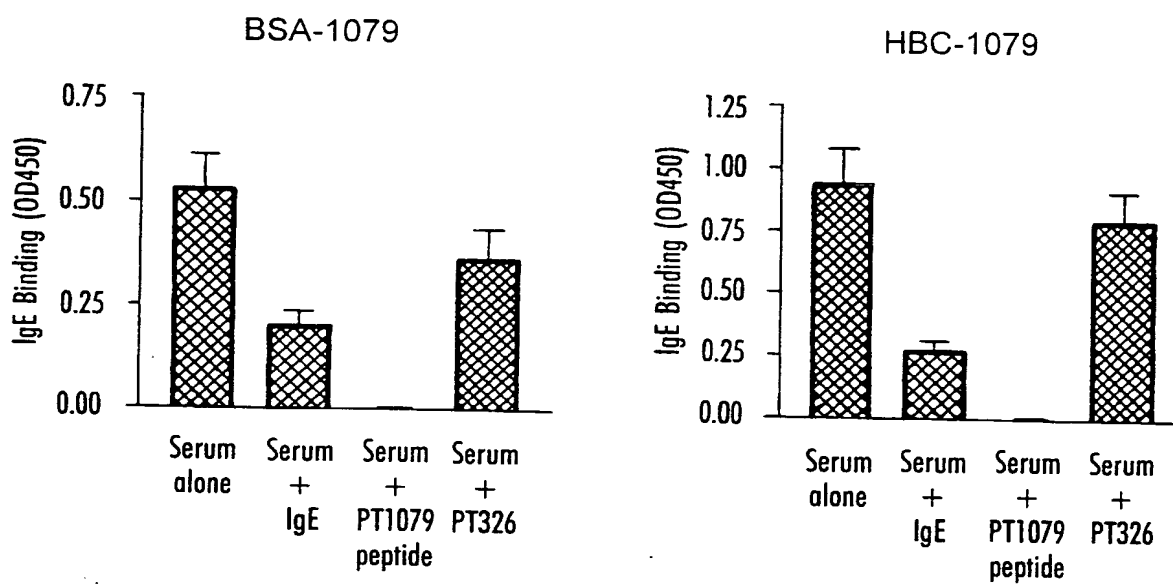


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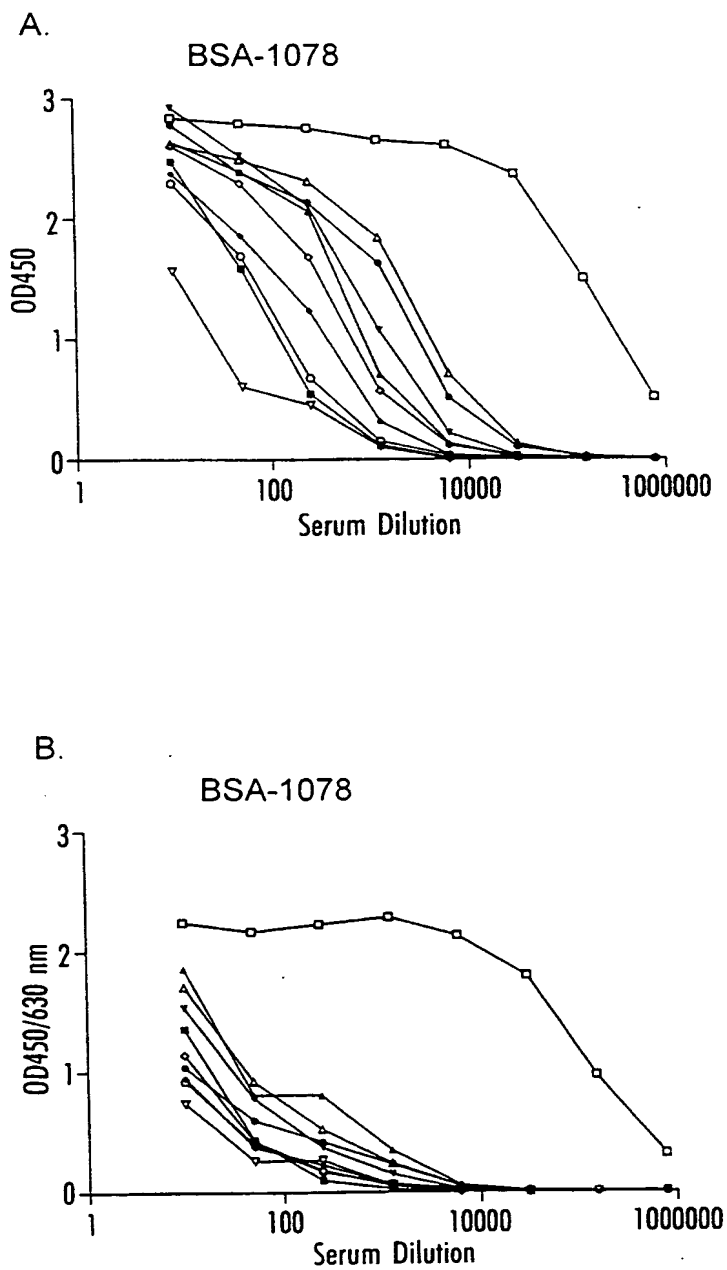
Fig. 7 PT1079 Anti-IgE Data

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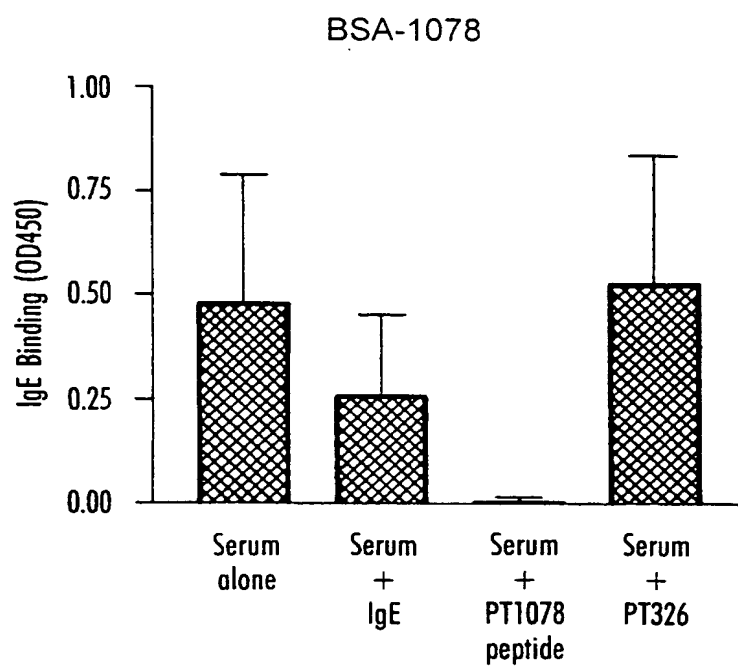
Fig. 8 Competition assay with soluble IgE and PT1079 peptide.



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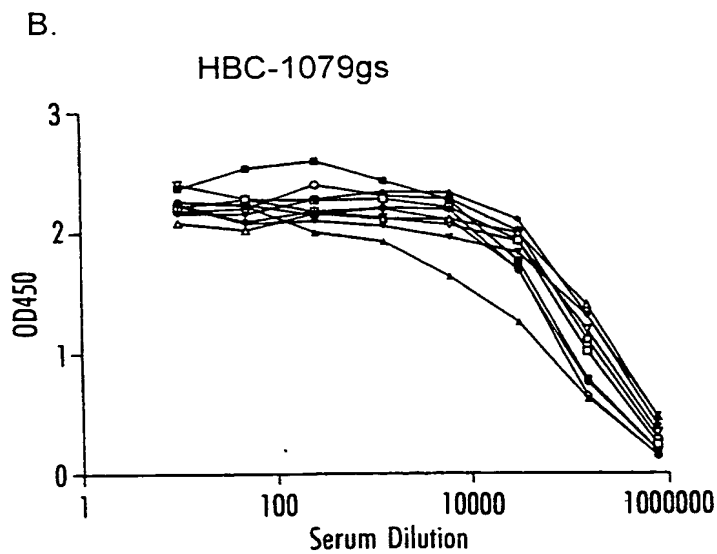
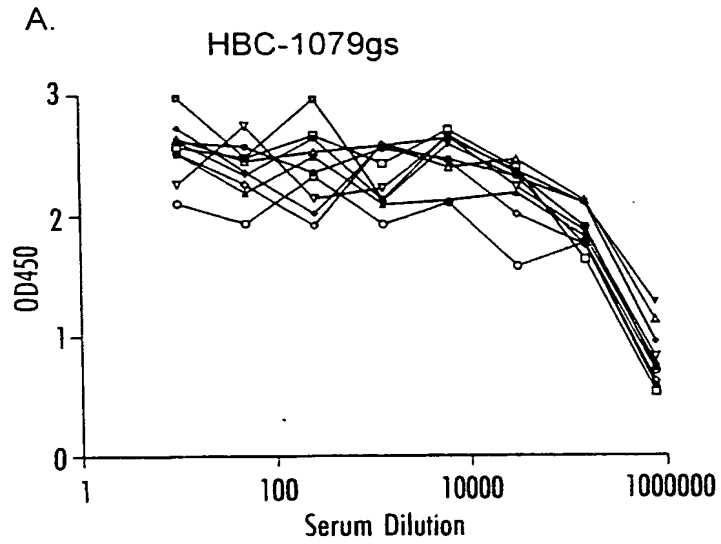
Fig. 9 PT1078 Anti-IgE Data

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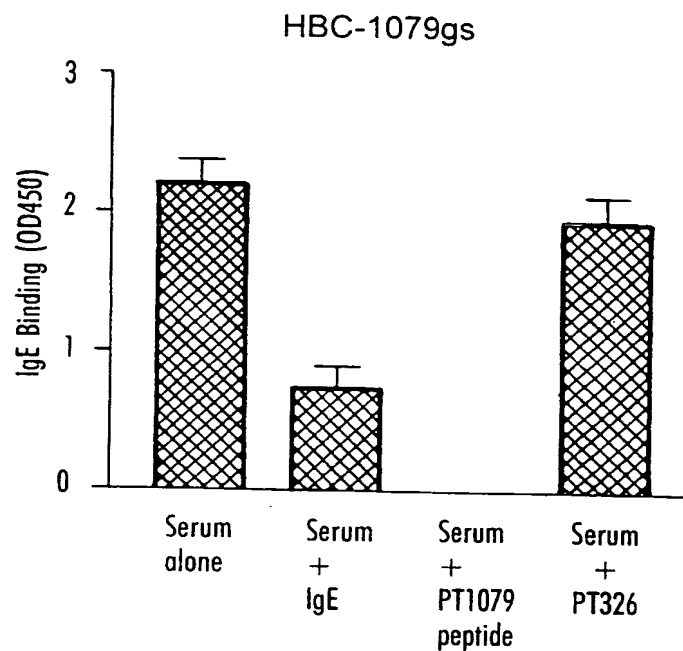
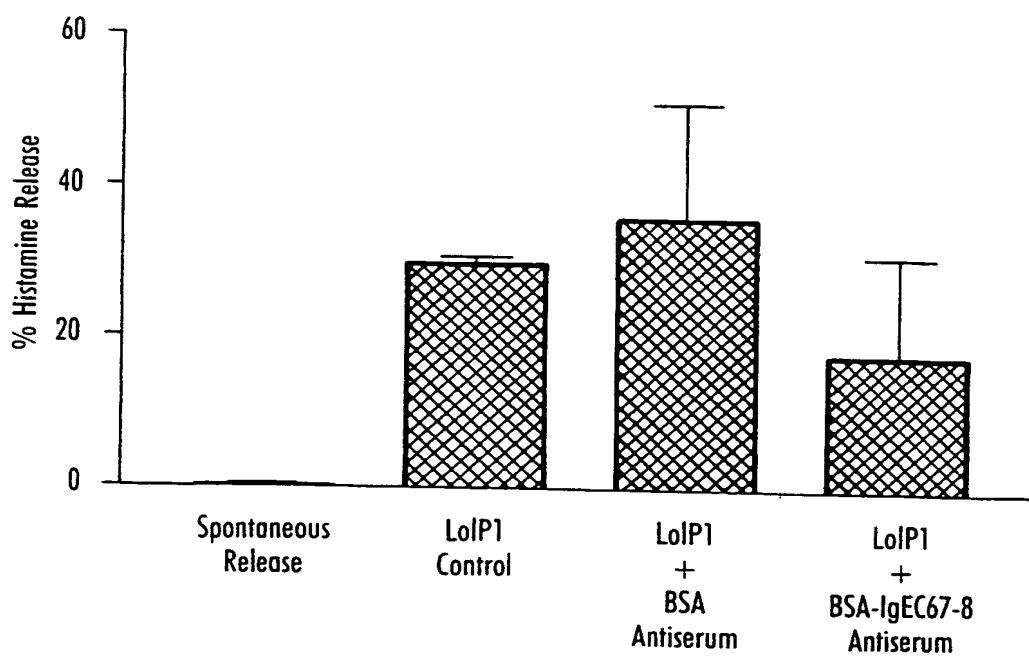
Fig. 10 Competition assay with soluble IgE and PT1078 peptide.

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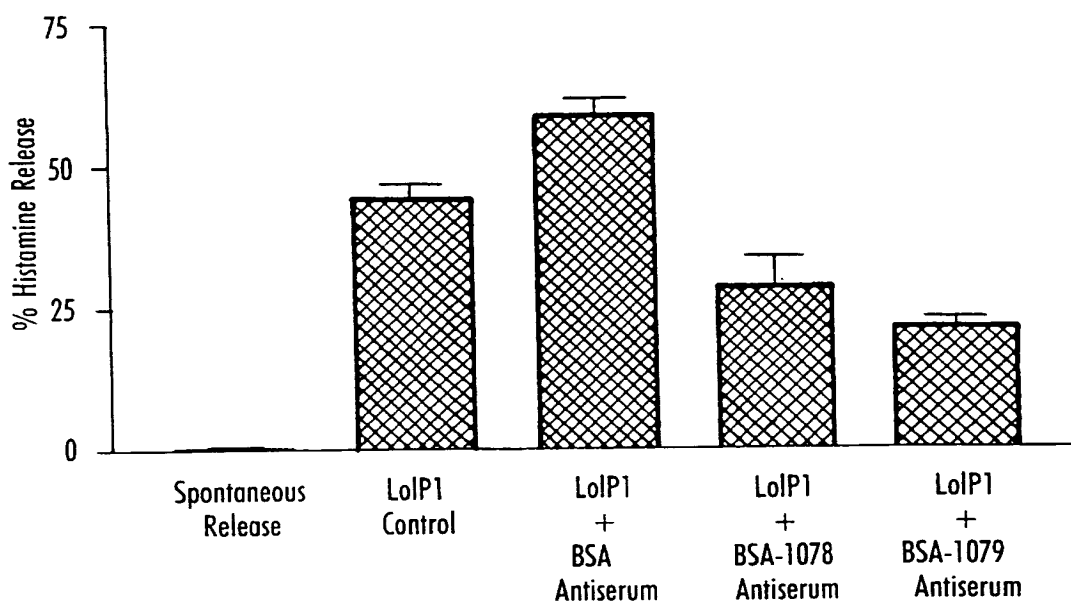
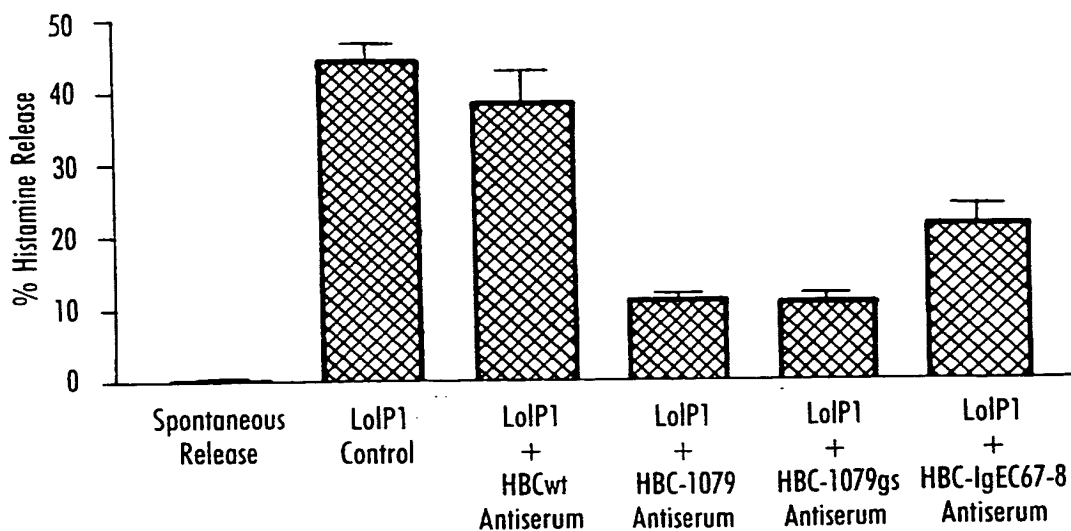
Fig. 11 PT1079gs Anti-IgE Data



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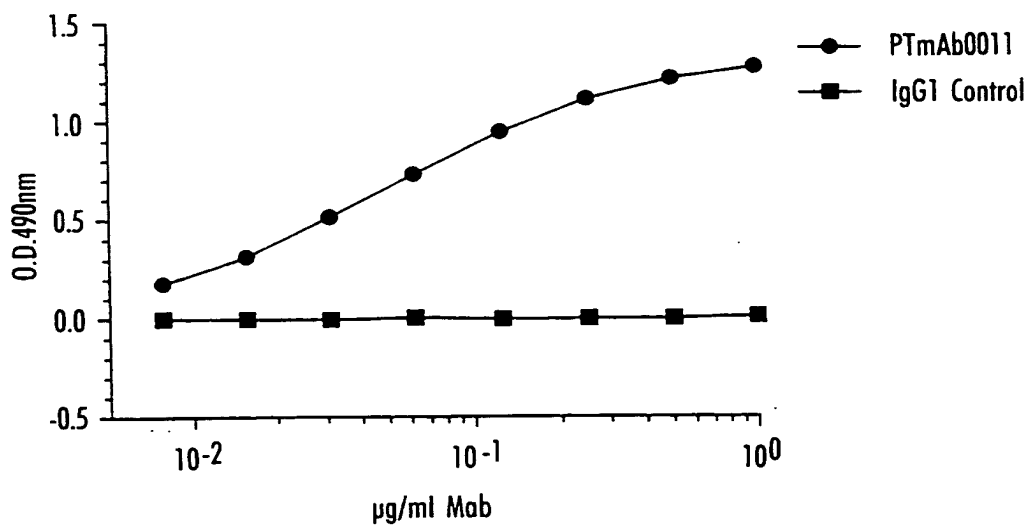
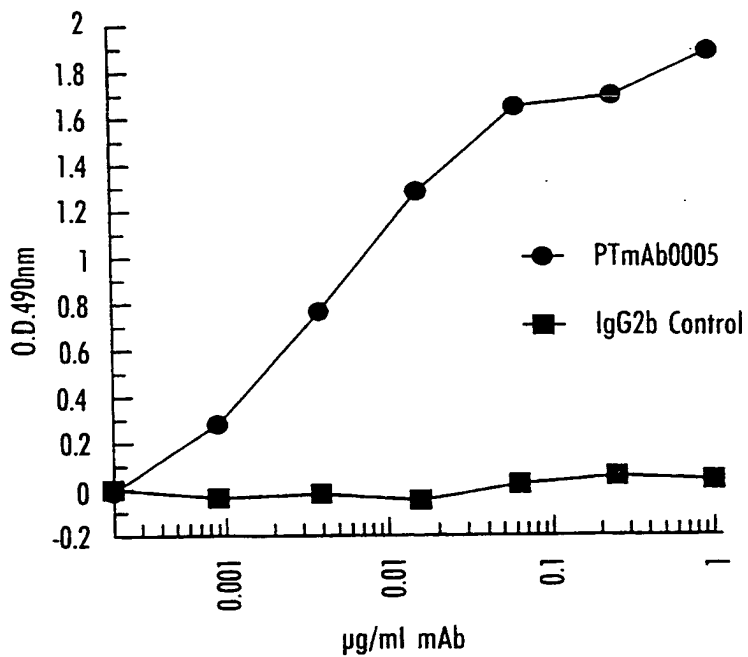
Fig. 12 Competition assay with soluble IgE and PT1079 peptide.**Fig. 13** Inhibitory Activity of Mouse BSA-C67-8 induced Antisera

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Fig. 14 Inhibitory Activity of Mouse Antisera induced by BSA-1078 and BSA-1079.**Fig.15** Inhibitory Activity of Mouse Antisera induced by HBC-C67-8, HBC-1078, HBC-1079 and HBC-1079gs

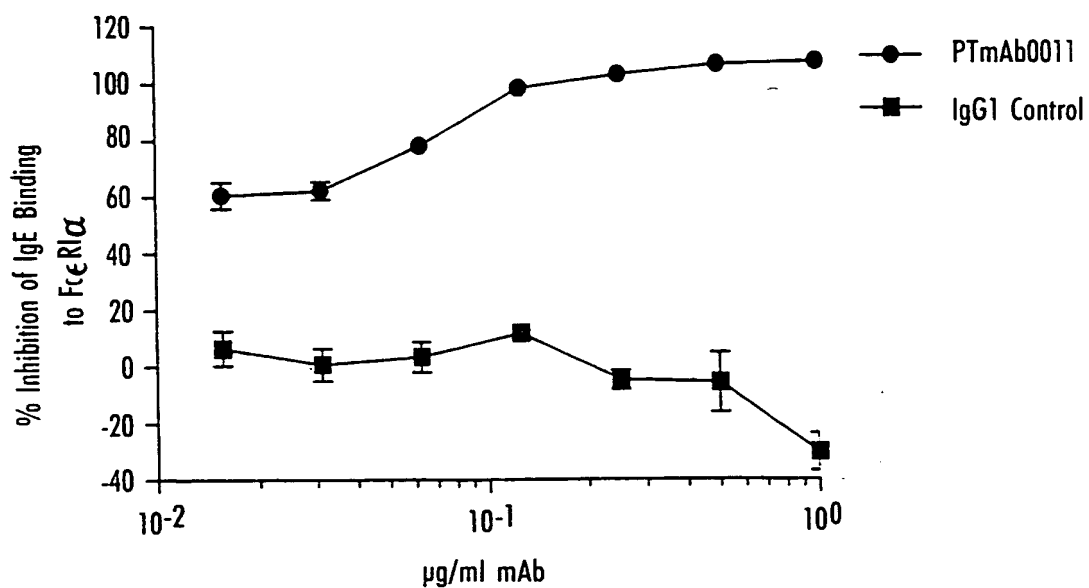
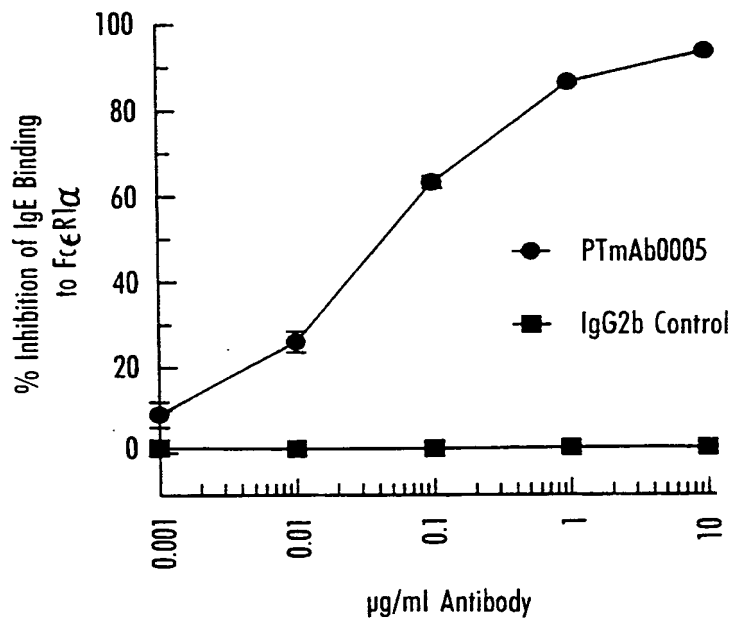
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Fig. 16 shows the concentration dependent binding of antibody PTmAb0005 and PTmAb0011 to IgE.



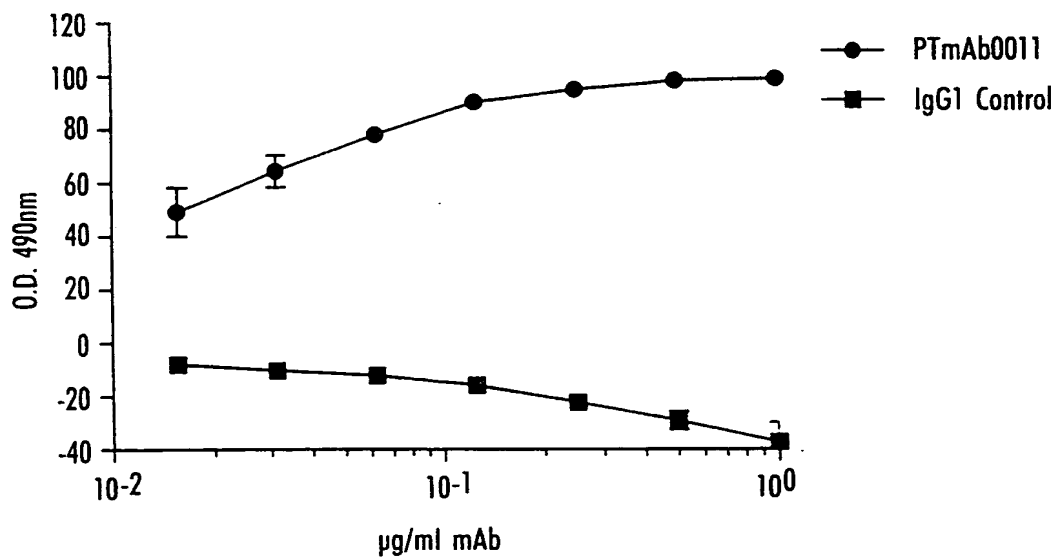
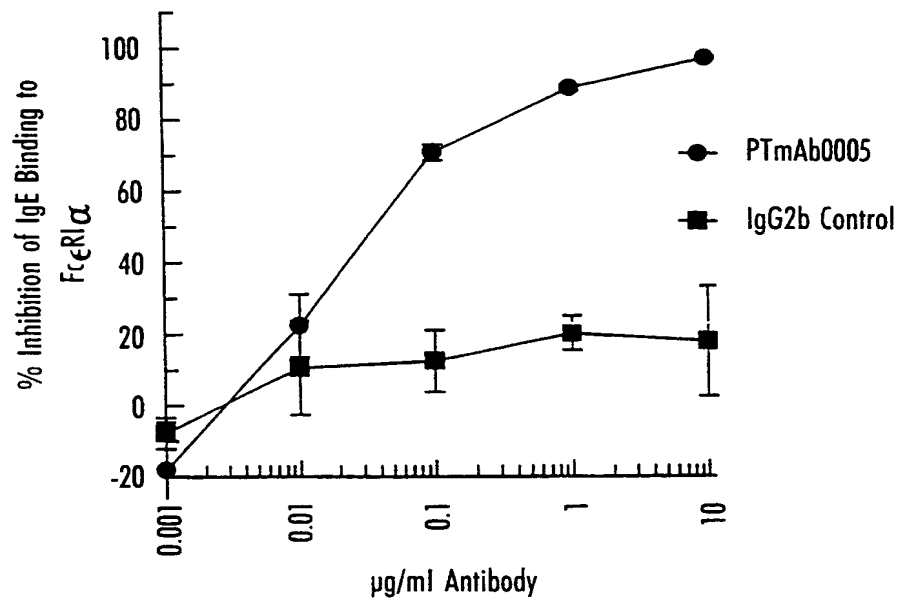
17/32

Fig. 17 shows the concentration dependent inhibition of IgE binding to an Fc ϵ R1 α /IgG construct with antibody PTmAb0005 and PTmAb0011 compared to control.



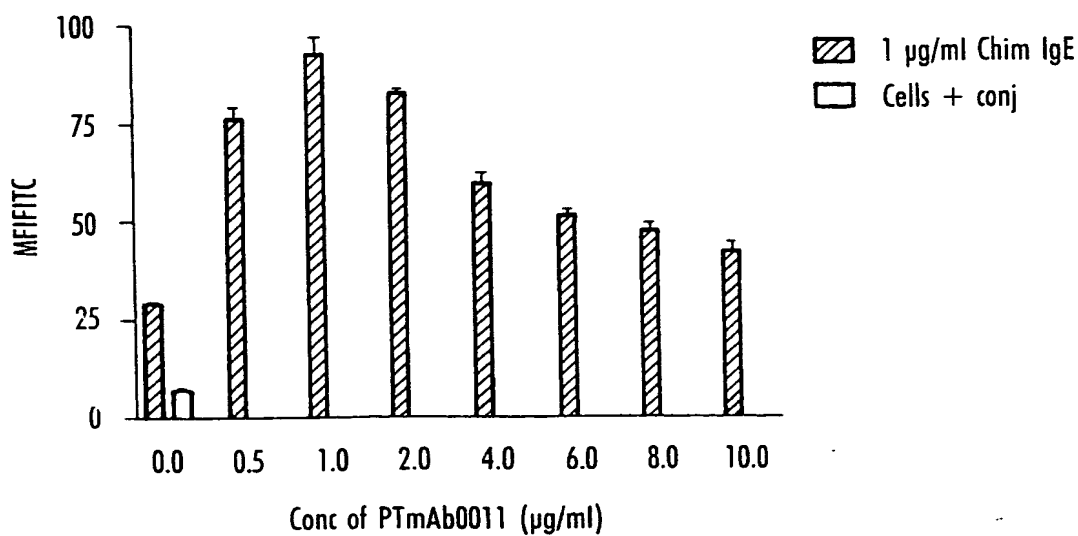
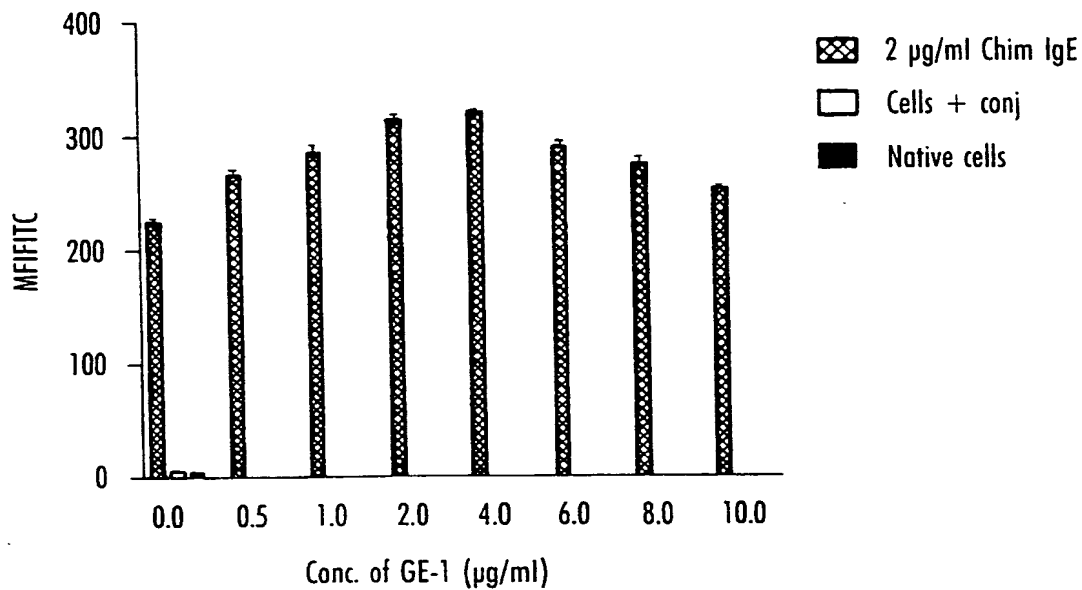
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Fig. 18 shows the concentration dependent inhibition of IgE binding to clipped ectodomain of Fc ϵ R1 α -bound directly to plastic plates, by antibody PTmAb0005, compared to control.



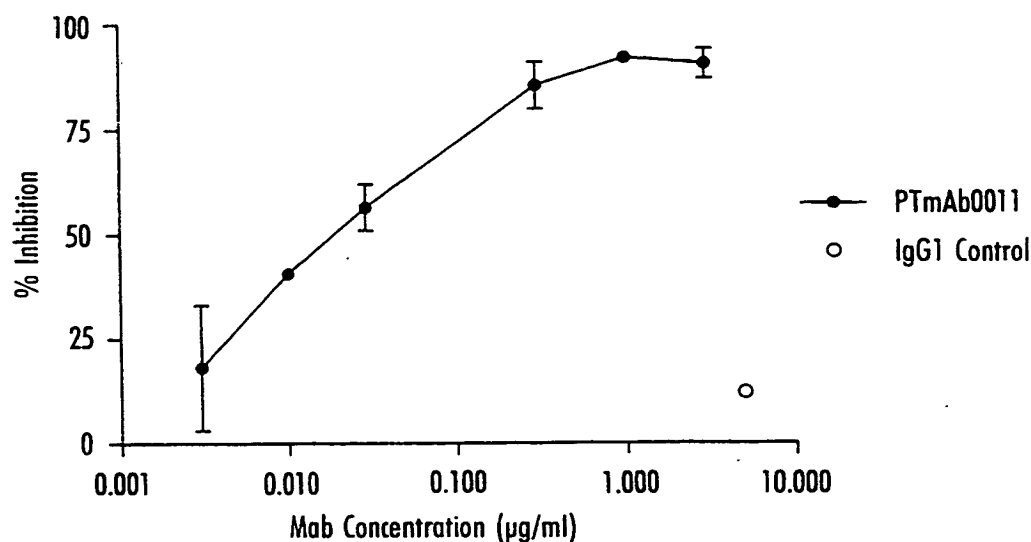
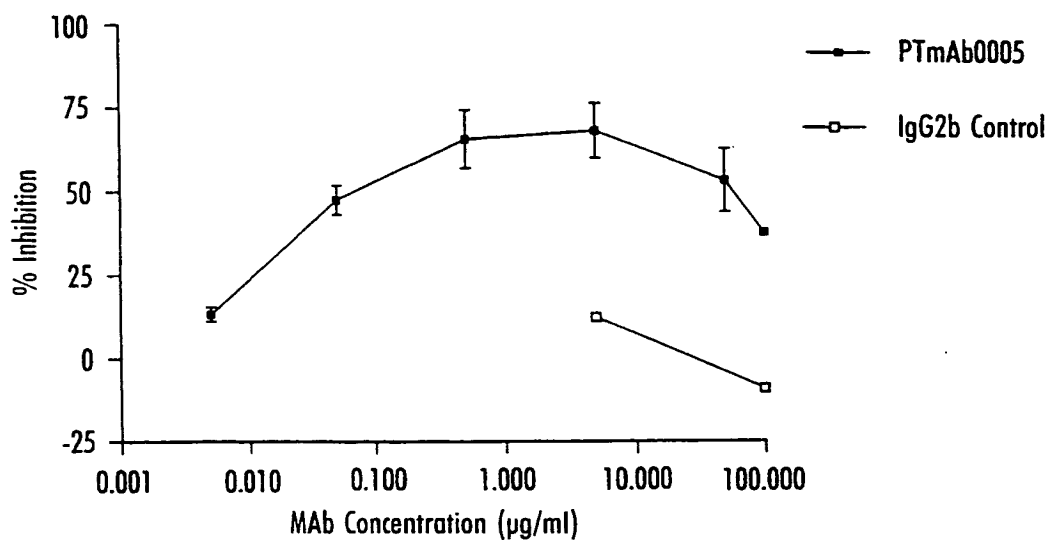
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Fig. 19 shows IgE binding to Fc ϵ RII (CD23) by antibody PTmAb0005 (GE-1) and PTmAb0011.



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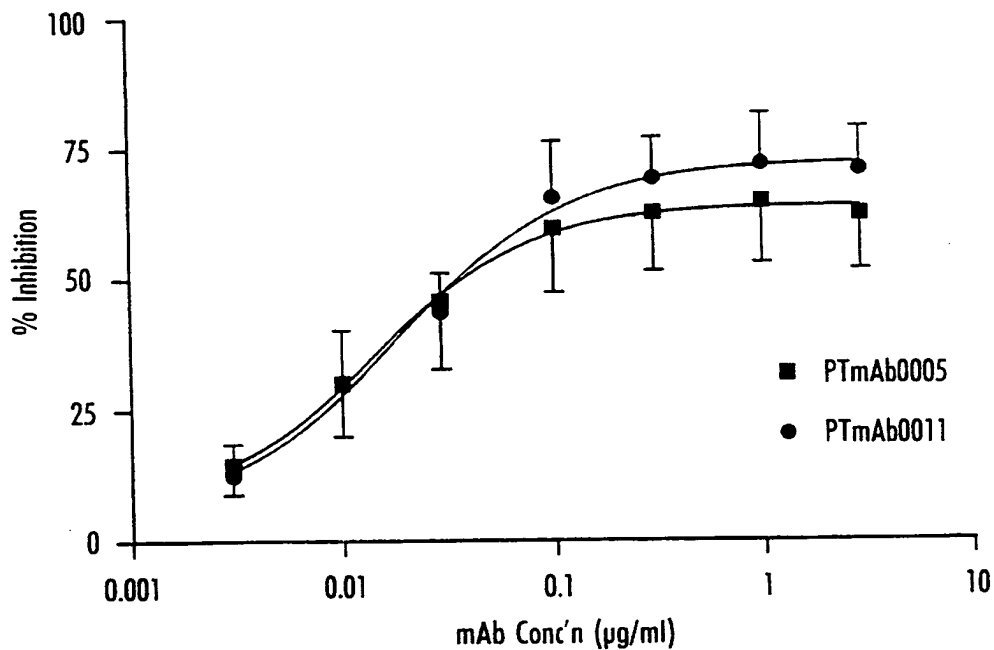
Fig. 20 shows the concentration-dependent blocking of histamine release from allergic human blood basophils with antibody PTmAb0005 and PTmAb0011 compared to control.



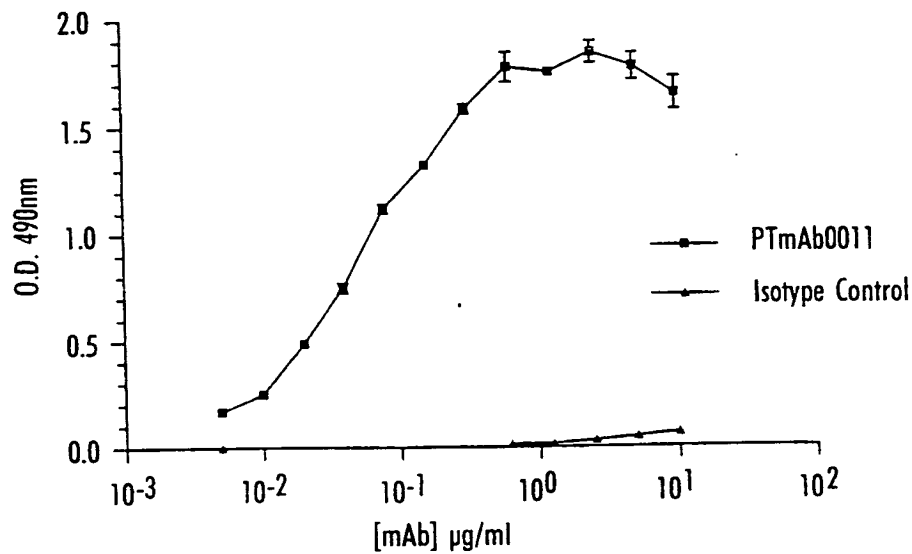
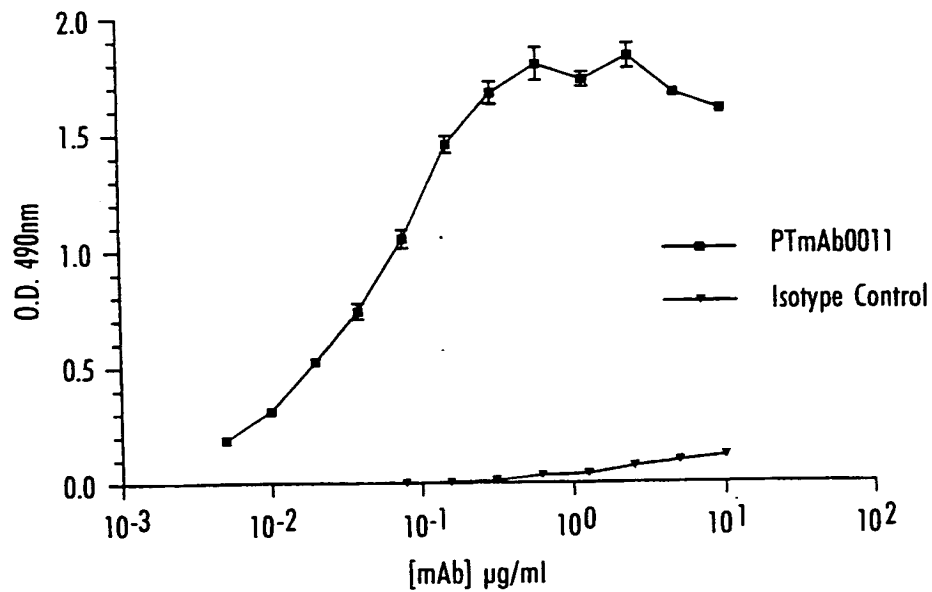
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Fig. 21

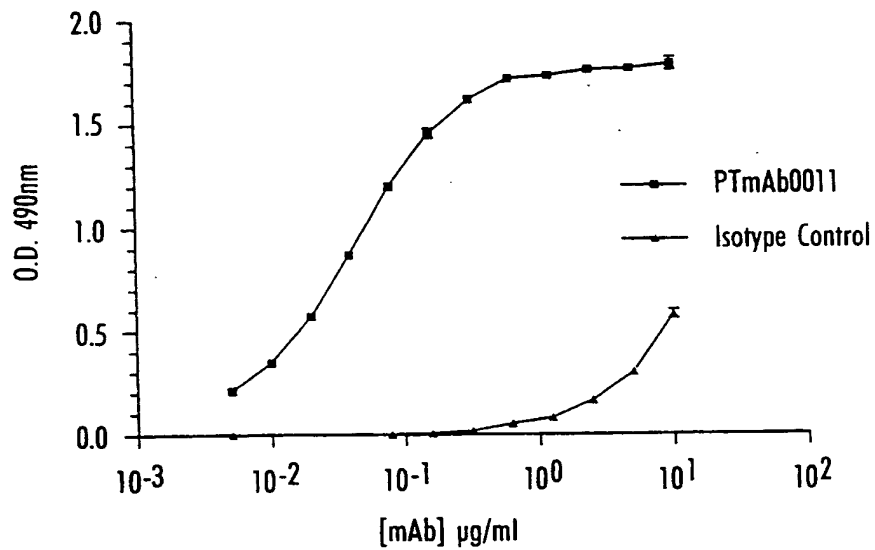
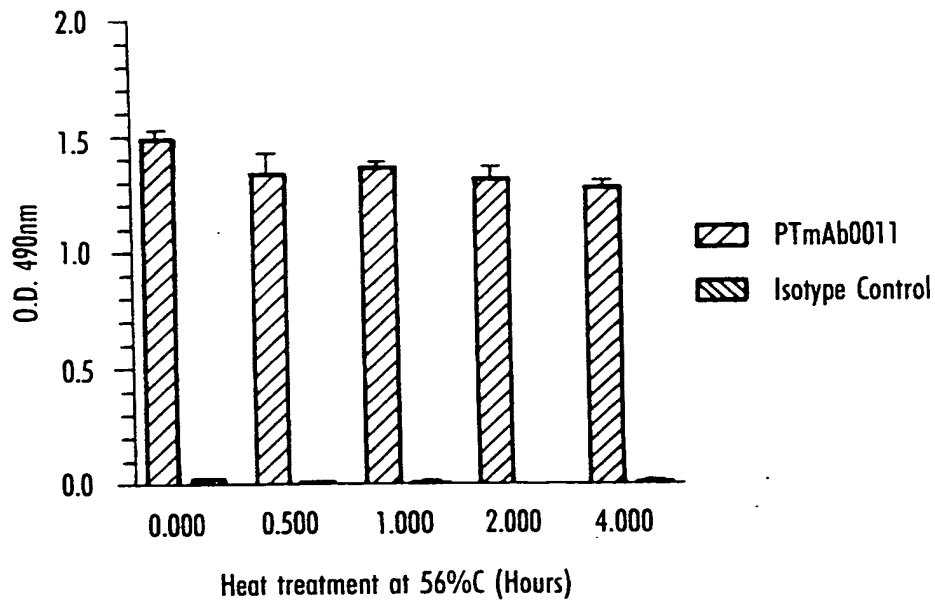
Inhibition of LolP1-Triggered
Histamine Release in Allergic
Human Basophils



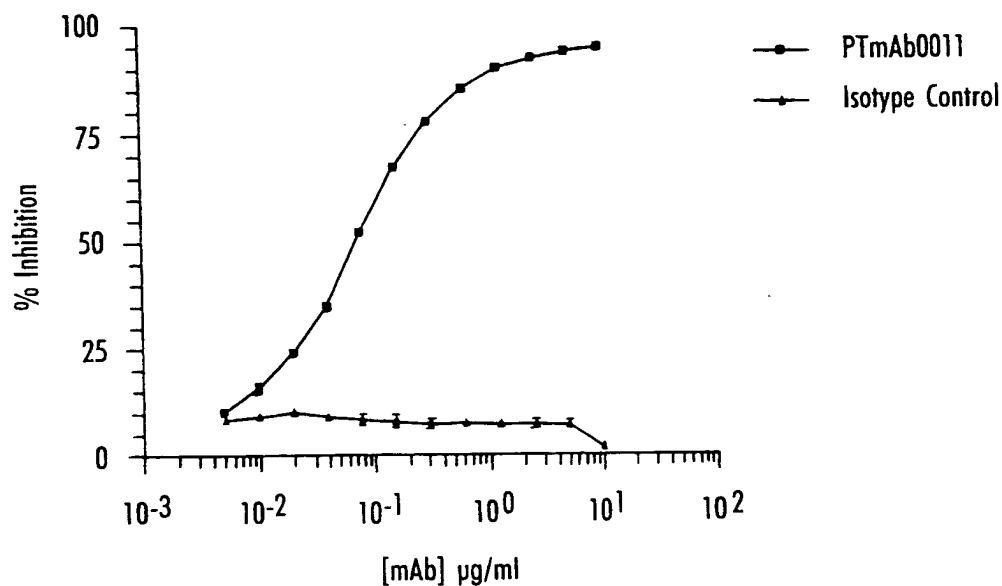
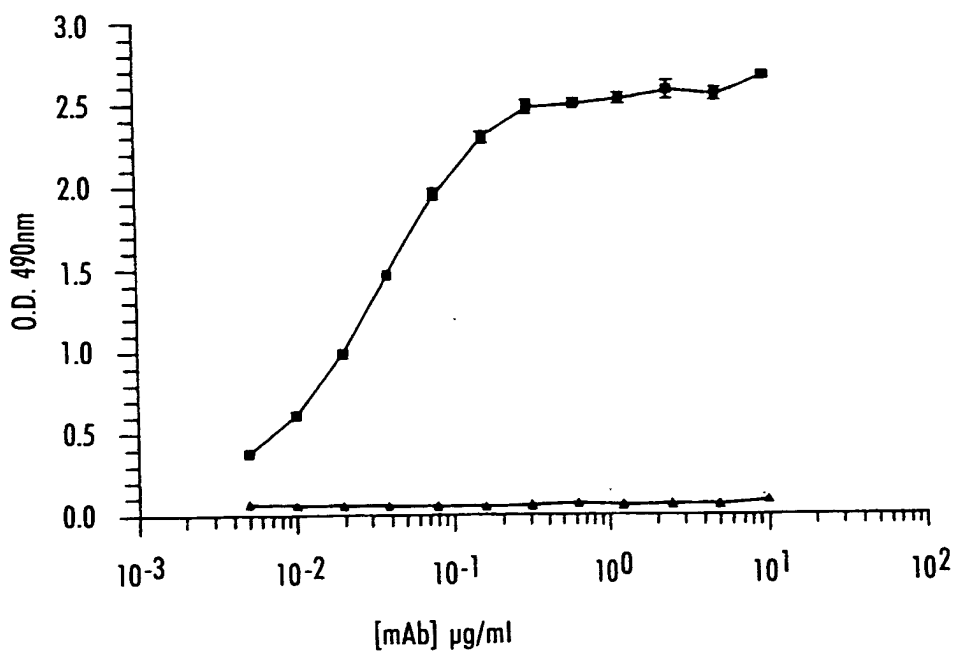
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Fig. 22 PTmAb0011 binding to different IgE.**A. Chimaeric IgE****B. Binding to Myeloma IgE**

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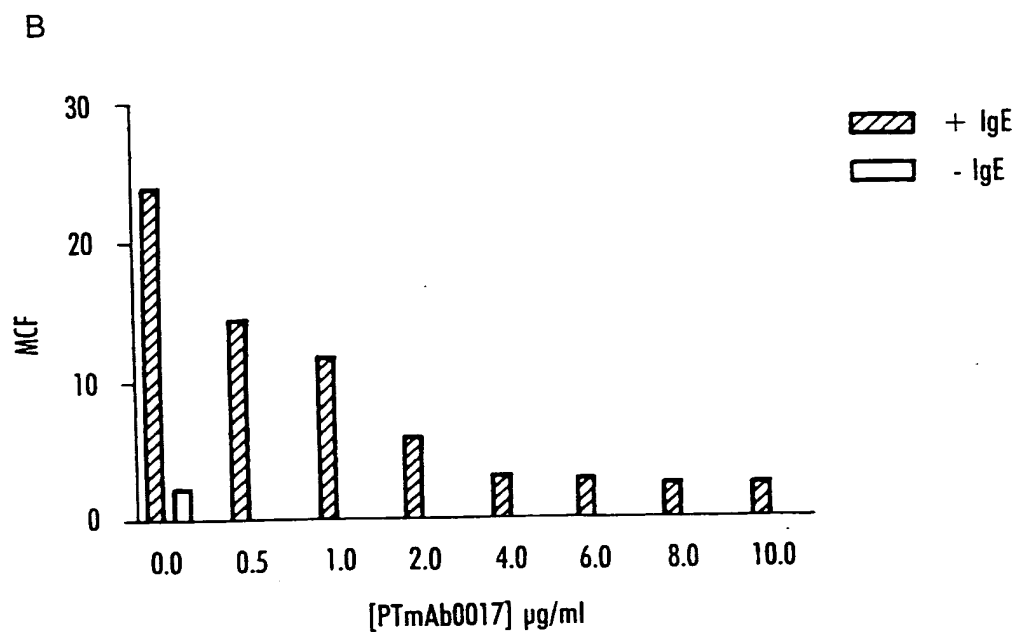
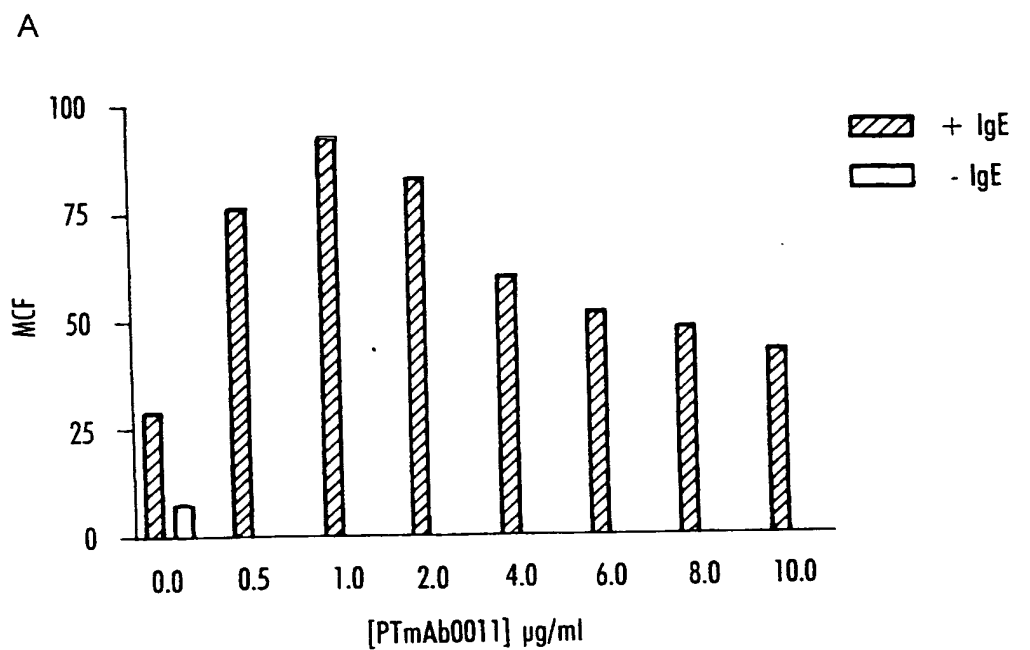
Fig. 22**C. Binding to Antigen Orientated IgE****D. Binding to Heat Denatured IgE**

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Fig. 23 Inhibition of IgE Binding to FcεR1α by PTmAb0011.**Fig. 24** Binding of PTmAb0011 to Receptor Bound IgE.

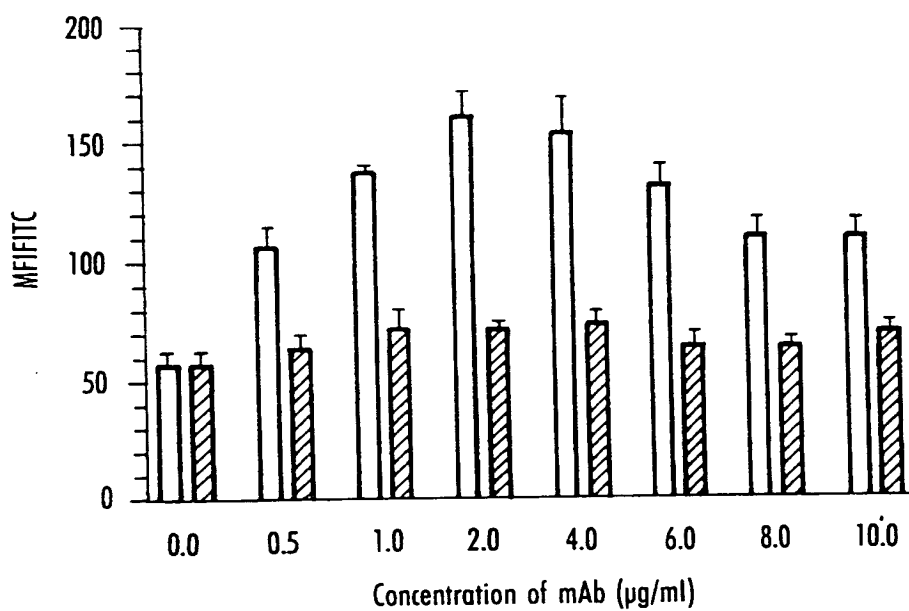
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Fig. 25 The effect of PTmAb0011 on IgE binding to FcεRII on RPMI 8866 cells.



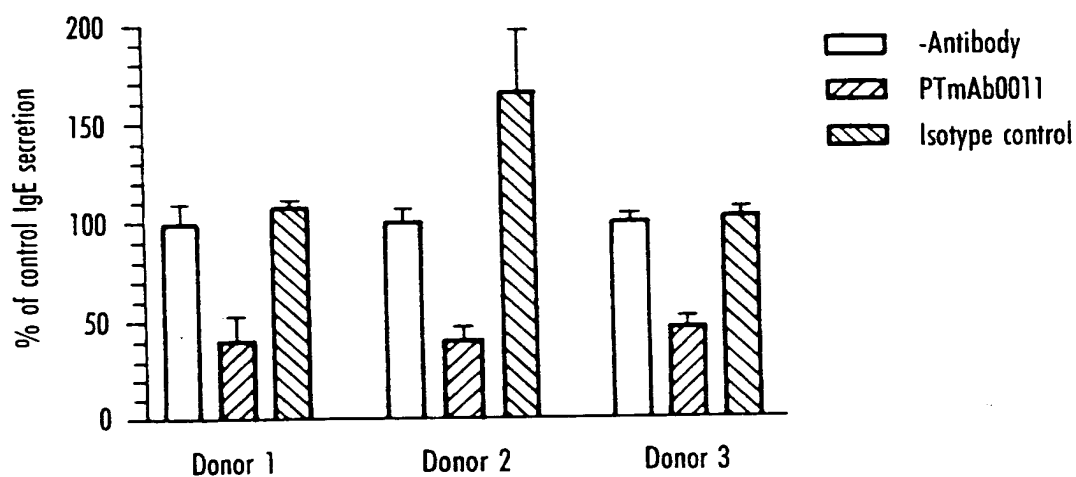
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Fig. 26 Analysis of the effects of PTmAb0011 on IgE binding to FcεRII on primary human B-cells.



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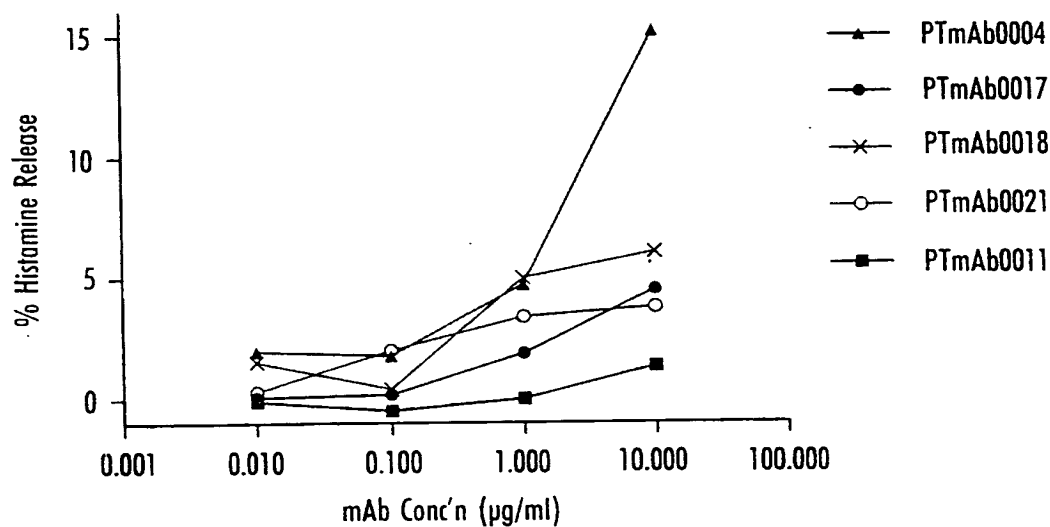
Fig. 27 Effects of PTmAb0011 on IgE secretion from primary human B-cells.



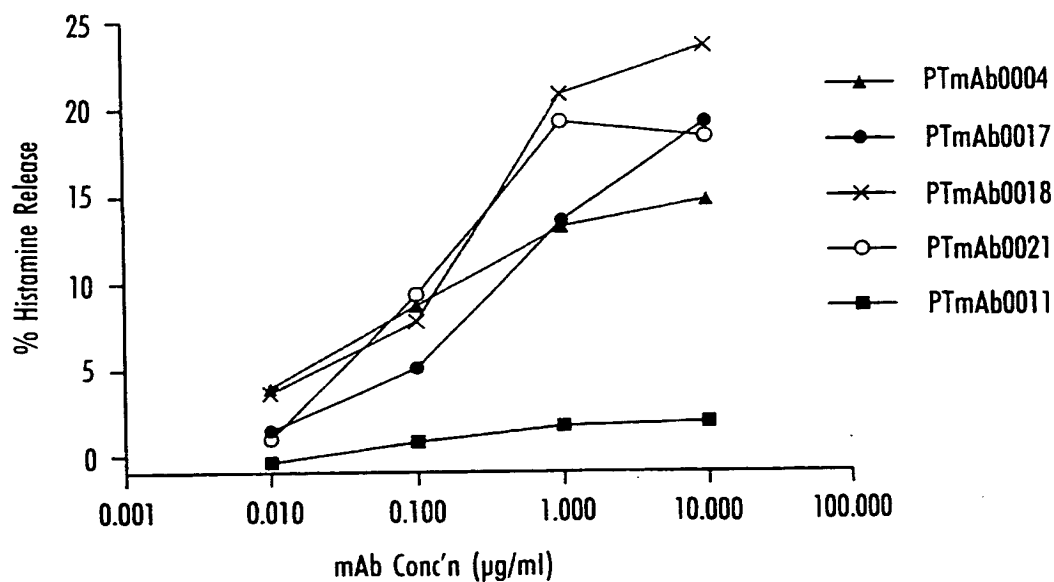
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Fig. 28 Anaphylactogenicity of anti-human IgE monoclonal antibodies in allergic (A) and non-allergic (B) human basophils

A

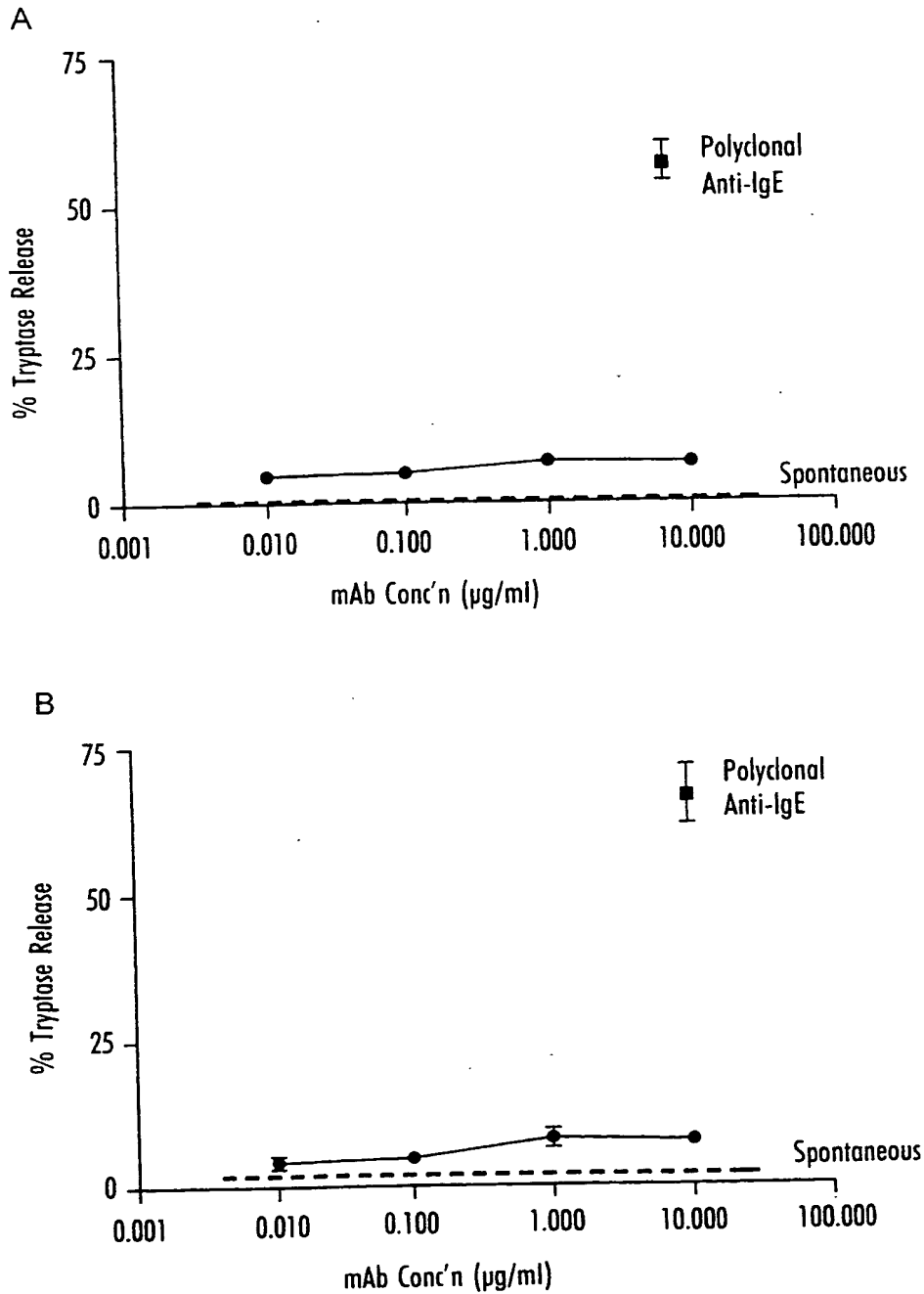


B



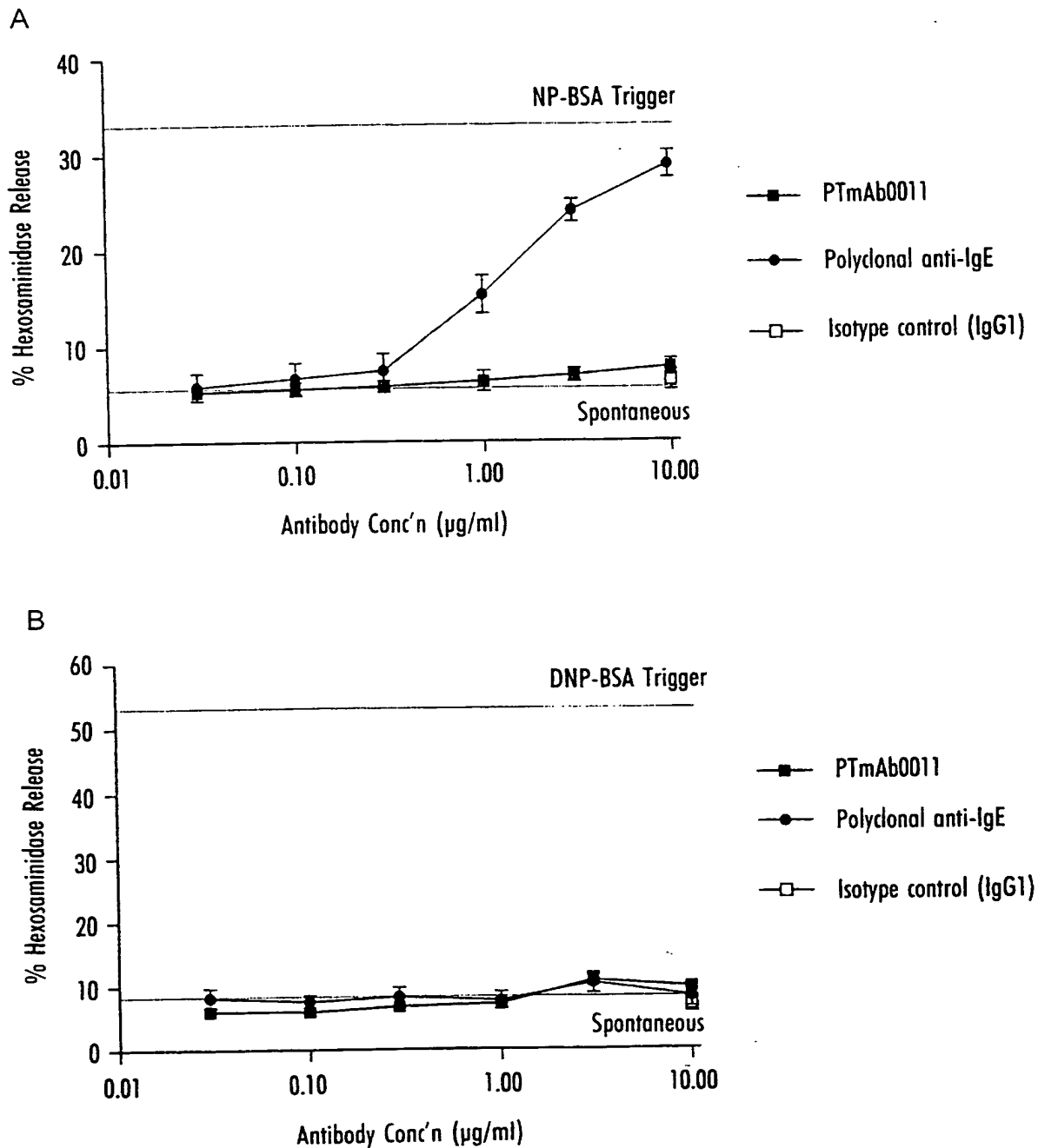
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Fig. 29 Anaphylactogenicity of anti-human IgE antibodies in sensitised (A) and non-sensitised (B) human lung mast cells



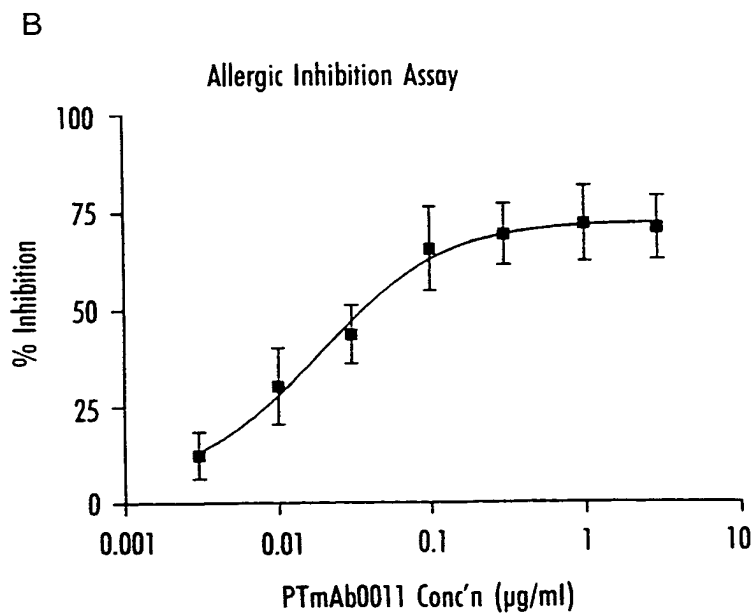
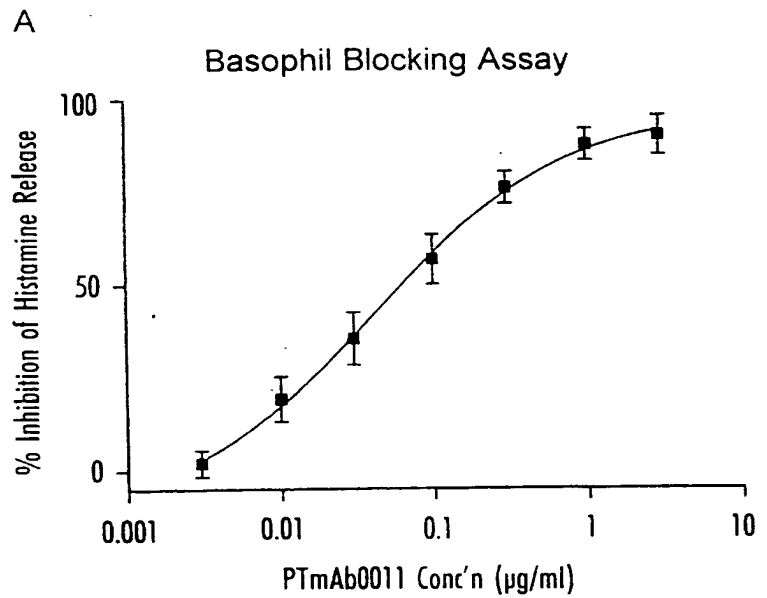
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Fig. 30 Anaphylactogenicity of anti-human IgE antibodies in RBL J41 cells through human FcεRI (A) and mouse FcεRI (B)



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Fig. 31 Inhibition of allergen-triggered histamine release in human basophils by PTmAb0011



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Fig. 32 Inhibition of passive cutaneous anaphylaxis in Monkey skin by PTmAb0011 and PTmAb0005.

